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START SEQ ID NO:1

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GCTGCGGAATTCTAATACGACTCACTATAGGGAGTCGACCCACGCGTCCGGTGGCAGGCCGGGTGAGGGCTCGCGC

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START SEQ ID NO:2

GTGGTCTCCTGCCGTGCCGGATCCCAGTCAGAAGTTCCAGCCTGCCACTGTTCTCTGATGCC ATG CCA GCA

START SEQ ID NO:3

P	T	Q	L	F	F	P	L	I	R	N	C	E	L	S	R	I	Y	G	T	
CCA	ACT	CAA	CTG	TTT	TTT	CCT	CTC	ATC	CGT	AAC	TGT	GAA	CTG	AGC	AGG	ATC	TAT	GGC	ACT	

3

9

A	C	Y	C	H	H	K	H	L	C	C	S	S	S	S	Y	I	P	Q	S	R
GCA	TGT	TAC	TGC	CAC	CAC	AAA	CAT	CTC	TGT	TGT	TCC	TCA	TCG	TAC	ATT	CCT	CAG	AGT	CGA	

43

129

L	R	Y	T	P	H	P	A	Y	A	T	F	C	R	P	K	E	N	W	W
CTG	AGA	TAC	ACA	CCT	CAT	CCA	GCA	TAT	GCT	ACC	TTT	TGC	AGG	CCA	AAG	GAG	AAC	TGG	TGG

63

189

Q	Y	T	Q	G	R	R	Y	A	S	T	P	Q	K	F	Y	L	T	P	P
CAG	TAC	ACC	CAA	GGA	AGG	AGA	TAT	GCT	TCC	ACA	CCA	CAG	AAA	TTT	TAC	CTC	ACA	CCT	CCA

83

249

Q	V	N	S	I	L	K	A	N	E	Y	S	F	K	V	P	E	F	D	G
CAA	GTC	AAT	AGC	ATC	CIT	AAA	GCT	AAT	GAA	TAC	AGT	TTC	AAA	GTG	CCA	GAA	TTT	GAC	GGC

103

309

K	N	V	S	S	I	L	G	F	D	S	N	Q	L	P	A	N	A	P	I
AAA	AAT	GTC	AGT	TCT	ATC	CTT	GGA	TTT	GAC	AGC	AAT	CAG	CTG	CCT	GCA	AAT	GCA	CCC	ATT

123

369

E	D	R	R	S	A	A	T	C	L	Q	T	R	G	M	L	L	G	V	F
GAG	GAC	CGG	AGA	AGT	GCA	GCA	ACC	TGC	TTG	CAG	ACC	AGA	GGG	ATG	CIT	TTG	GGG	GTT	TTT

143

429

D	G	H	A	G	C	A	C	S	Q	A	V	S	E	R	L	F	Y	Y	I
GAT	GGC	CAT	GCA	GGT	TGT	GCT	TGT	TCC	CAG	GCA	GTC	AGT	GAA	AGA	CTC	TTT	TAT	TAT	ATT

163

489

A	V	S	L	L	P	H	E	T	L	L	E	I	E	N	A	V	E	S	G
GCT	GTC	TCT	TTG	TTA	CCC	CAT	GAG	ACT	TTG	CTA	GAG	ATT	GAA	AAT	GCA	GTG	GAG	AGC	GGC

183

549

R	A	L	L	P	I	L	Q	W	H	K	H	P	N	D	Y	F	S	K	E
CGG	GCA	CTG	CTA	CCC	ATT	CTC	CAG	TGG	CAC	AAG	CAC	CCC	AAT	GAT	TAC	TTT	AGT	AAG	GAG

203

609

A	S	K	L	Y	F	N	S	L	R	T	Y	W	Q	E	L	I	D	L	N
GCA	TCC	AAA	TTG	TAC	TTT	AAC	AGC	TTG	AGG	ACT	TAC	TGG	CAA	GAG	CIT	ATA	GAC	CTC	AAC

223

669

T	G	E	S	T	D	I	D	V	K	E	A	L	I	N	A	F	K	R	L
ACT	GGT	GAG	TCG	ACT	GAT	ATT	GAT	GTT	AAG	GAG	GCT	CTA	ATT	AAT	GCC	TTC	AAG	AGG	CIT

243

729

D	N	D	I	S	L	E	A	Q	V	G	D	P	N	S	F	L	N	Y	L
GAT	AAT	GAC	ATC	TCC	TTG	GAG	GCG	CAA	GTT	GGT	GAT	CCT	AAT	TCT	TTT	CTC	AAC	TAC	CTG

263

789

V	L	R	V	A	F	S	G	A	T	A	C	V	A	H	V	D	G	V	D
GTG	CIT	CGA	GTG	GCA	TTT	TCT	GGA	GCC	ACT	GCT	TGT	GTG	GCC	CAT	GTG	GAT	GGT	GTT	GAC

283

849

L	H	V	A	N	T	G	D	S	R	A	M	L	G	V	Q	E	E	D	G
CIT	CAT	GTG	GCC	AAT	ACT	GGC	GAT	AGC	AGA	GCC	ATG	CTG	GGT	GTG	CAG	GAA	GAG	GAC	GGC

303

909

S W S A V T L S N D H N A Q N E R E L E 323
 TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA 969

R L K L E H P K S E A K S V V K Q D R L 343
 CGG CTG AAA TTG GAA CAT CCA AAG AGT GAG GCC AAG AGT GTC GTG AAA CAG GAT CGG CTG 1029

L G L L M P F R A F G D V K F K W S I D 363
 CTT GGC TTG CTG ATG CCA TTT AGG GCA TTT GGA GAT GTA AAG TTC AAA TGG AGC ATT GAC 1089

L Q K R V I E S G P D Q L N D N E Y T K 383
 CTT CAA AAG AGA GTG ATA GAA TCT GGC CCA GAC CAG TTG AAT GAC AAT GAA TAT ACC AAG 1149

F I P P N Y H T P P Y L T A E P E V T Y 403
 TTT ATT CCT CCT AAT TAT CAC ACA CCT CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC 1209

H R L R P Q D K F L V L A T D G L W E T 423
 CAC CGA TTA AGG CCA CAG GAT AAG TTT CTG GTG TTG GCT ACT GAT GGG TTG TGG GAG ACT 1269

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 ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA 1329

Q P I A V G G Y K V T L G Q M H G L L T 463
 CAG CCA ATA GCT GTT GGT GGC TAC AAG GTG ACT CTG GGA CAG ATG CAT GGC CTT TTA ACA 1389

E R R T K M S S V F E D Q N A A T H L I 483
 GAA AGG AGA ACC AAA ATG TCC TCG GTA TTT GAG GAT CAG AAC GCA GCA ACC CAT CTC ATT 1449

R H A V G N N E F G T V D H E R L S K M 503
 CGC CAC GCT GTG GGC AAC AAC GAG TTT GGG ACT GTT GAT CAT GAG CGC CTC TCT AAA ATG 1509

L S L P E E L A R M Y R D D I T I I V V 523
 CTT AGT CTT CCT GAA GAG CTT GCT CGA ATG TAC AGA GAT GAC ATT ACA ATC ATT GTA GTT 1569

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Fig. 1B

PROTEIN PHOSPHATASE 2C DOMAIN

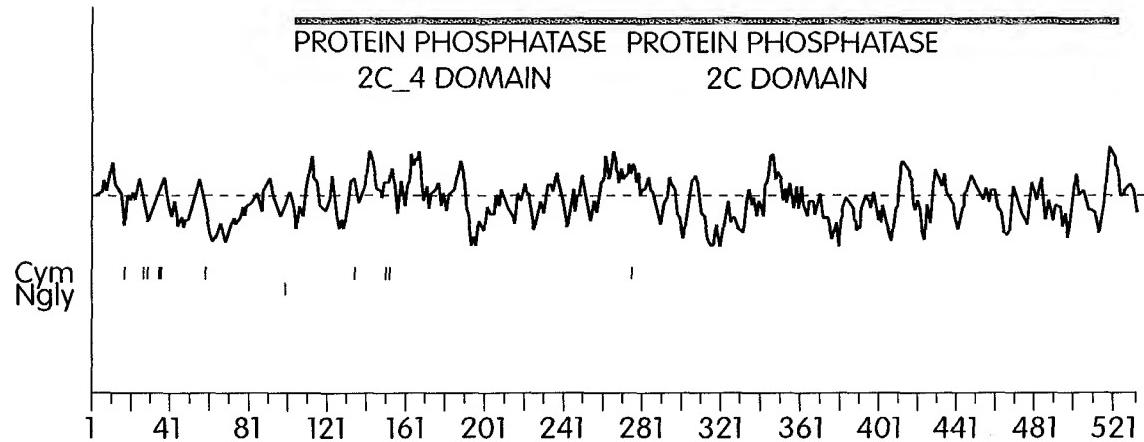


Fig. 2

PP2C: domain 1 of 1, from 173 to 461; score 261.3, E = 1.3e-74

*->1dvqvsrmqqwrksmeDahialknlnsssgkdswsffavfDGhgGs SEQ ID NO:4

1 +++++ + r +++ ++++++ ++ s++ s+ +f +++ +
26583 173 LLETEENAVESGRALLPTILOWHKHPNDYF-SKEASKLYFNSLRTYWOE 218 SEQ ID NO:2

qaakyagkhlhk.tilaerksfpegdpwEmk1sdledalkesfleadtde
+ +att ttt + att f+ +dt d + +ttt ++++++

26583 219 LIDLNTGESTDIDVKEALINAFKRLDN-----DISLEAQVGDPNSFLNY 262

elrsaesaankvlkedlssGsTAvalirgnkLyVANvGDSRaVlcrn
+++ + SG+TA+va+++q +L+VAN+GDSRa+L+ +

26583 263 LVL.R-----VAEFGATACVAHVDGVDLHVANTGDSRAML.GVO 299

gnaikw.avtLteDHkPsnedEreR!eaGGFvsrvs...ngRvnGvLav
+++++W+avtL++DH+++ne+E+eR++ +++++ + +s +--+R++G L++

26583 300 EEDGSWsAVTL SNDHNAONERELERLKL EHPKSEAKSVV kODRLLGLLMP 349

SRAfGDfelKpgsklgpeas.l.e.a.ny.eyiks.pe....qlVtaeP
RAfGD+++K+ +l+++ ++++++ n++ey+k+ p++ +++++ taeP

26583 350 FRAFGDVFKWSIDLOKRVTeSqPdOlNDnEYTKEfPPnyhttpPYLTAEIP 399

dvtssstdltpdkDeFlilAcDGLWDvvsdqevvdivrselsdgnksaedp
+yt ++l+p+ D+Fl+LA+DGLW++++ q+vv iv + l+ + +

26583 400 FVT-YHRLRPO-DKELVLTADGLWETMHRDVVRIVGEYL.TGM-----H 441

meaaeklvdeaiargaeDni<-*

++ ++ + + g ++
26583 442 HOPIAVGGYKVTLGOMHGL 461

Fig. 3A

PP2C_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98

*->es.sgknlglyglgessmgwrkpmEDahvirp.....ffgvfD SEQ ID NO:5

+ gkn +++ g+ +s++ +++ p+ED+ ++ + +++++ + gVfd

26583 99 PEFDGKVNSSLGF-DSNQLPANAPIEDRRSAATclqtrgmLLGVFD 144 SEQ ID NO:2

GHGGseaakflsknlheilaeelsfdkdeslkene.e.lk.d.ep....

GH+G +++ +s++l+ ++a +l +++ + en+ e+++ + ++ + ++

26583 145 GHAGCACSQAVSERLFYYIAVSLLPHETLLEIENAvEsGRaLLPIlqwnk 194

.....ess.e.r.ln.gdksledveealrkaFlrttd

++++ +++ ++ ++ ++++++e +ln+g++++ dv+eal++aF+r+d

26583 195 hpndyfskeasklyfnslrTYWqElIdLNtGESTDIDVKEALINAFKRLD 244

eei.....stAvvalirgnklyvANvGDSRa

++i+ + + +++++ + + + +TA+va+++g +l+vAN+GDSRa

26583 245 NDIsleaqvgdponsflnylvrvafsgATACVAHVGDVLDLVANTGDSRA 294

vLcrngkd.swegvrtyssavqlteDHkpanedEreRieaaGGevepidre

+L+ + +d+sw sav L++DH++ ne+E+eR++ +++++ e +++

26583 295 MLGVQEEDgSW-----SAVTLSNDHNAQNEREELERLKLEHPKSE--AKS 336

fvsngggvvwRvnGvvisLavsRalGDfelKk.ked.e.lie....en.

+v ++ R++G L++ Ra+GD+++K+++++++=ie+++++n+

26583 337 VVKQD----RLLGL---LMPFRAFGDVFKWsIDLqKrVIEsgpdqLNd 378

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26583 379 NEYTKFIPPNYHTPPYLTAEPETYHRL-----RPQDKFLVLATDGLWE 422

vlsnqeavdivrkhlrkgsdk.evksaaqela.r.a.d....s.....

+ q++v iv + l+++++ +++++ +++++ +++++ ++

26583 423 TMHRQDVVRIVGEYLTGMHHQqPIAVGGYKVTLGqMhGllteRrtkmssv 472

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++++ ++l r+ +++++ +++L +++ +++ + +D+iT++v

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v<-*

v

26583 523 V 523

Fig. 3B

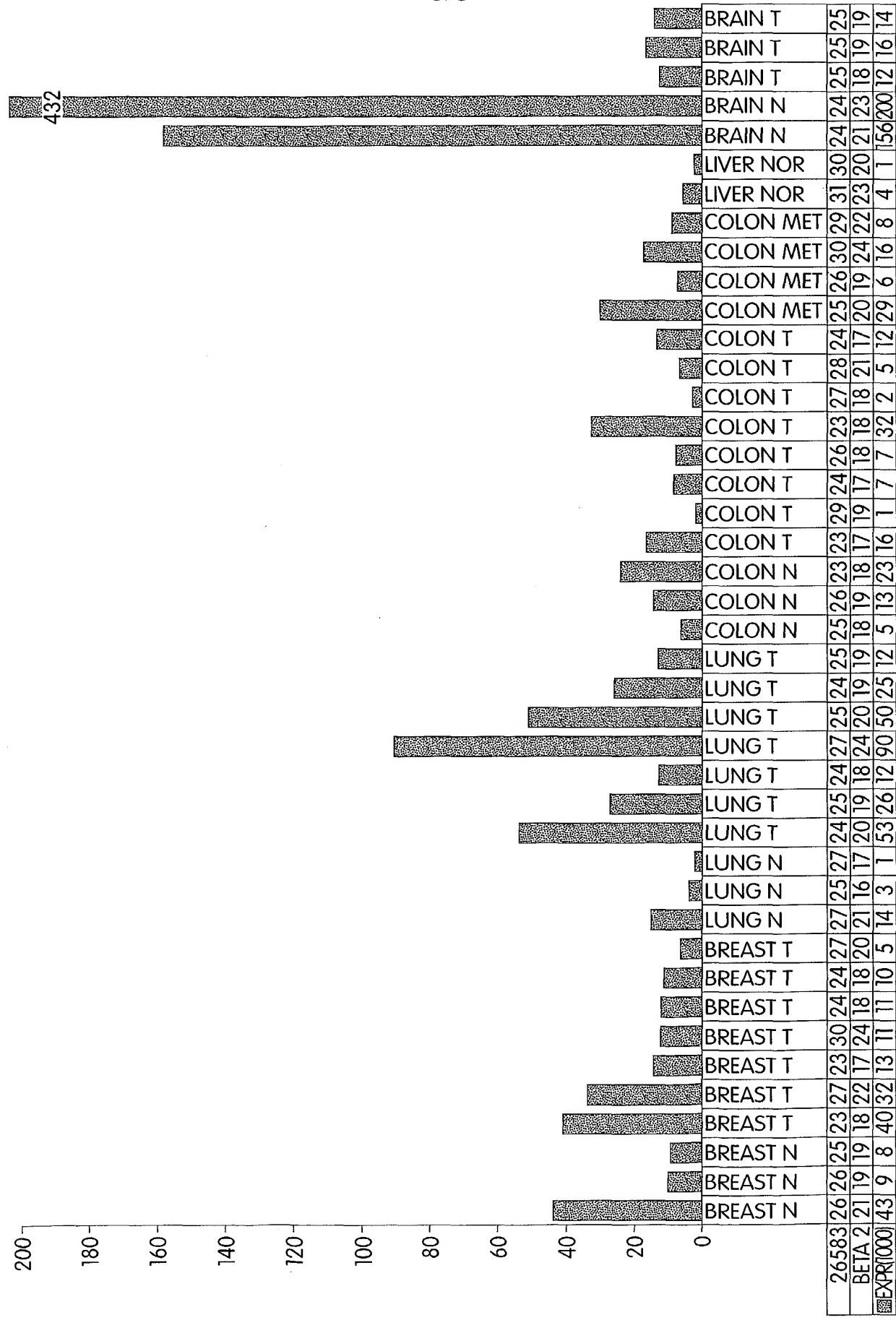


Fig. 4